

FIG. 1A

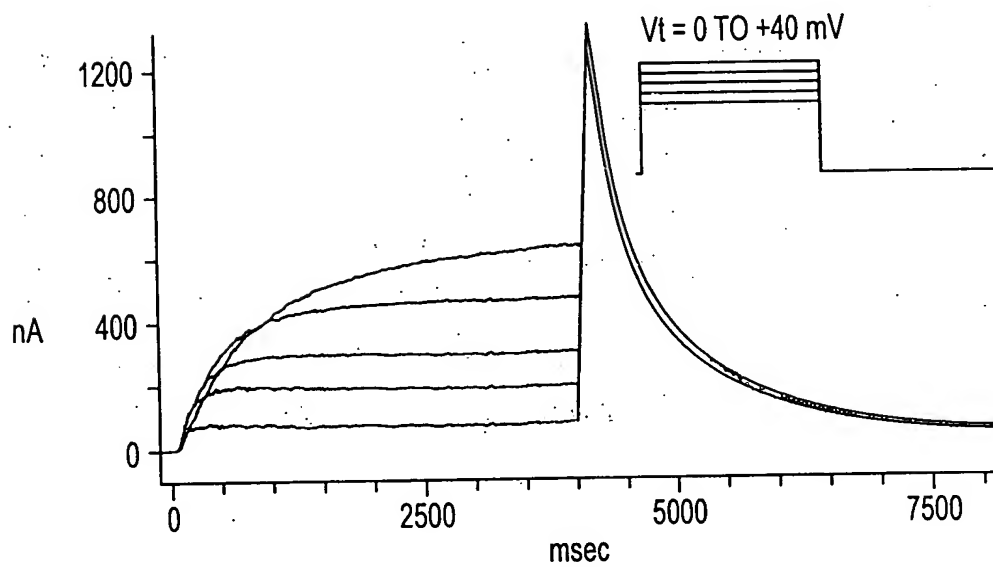
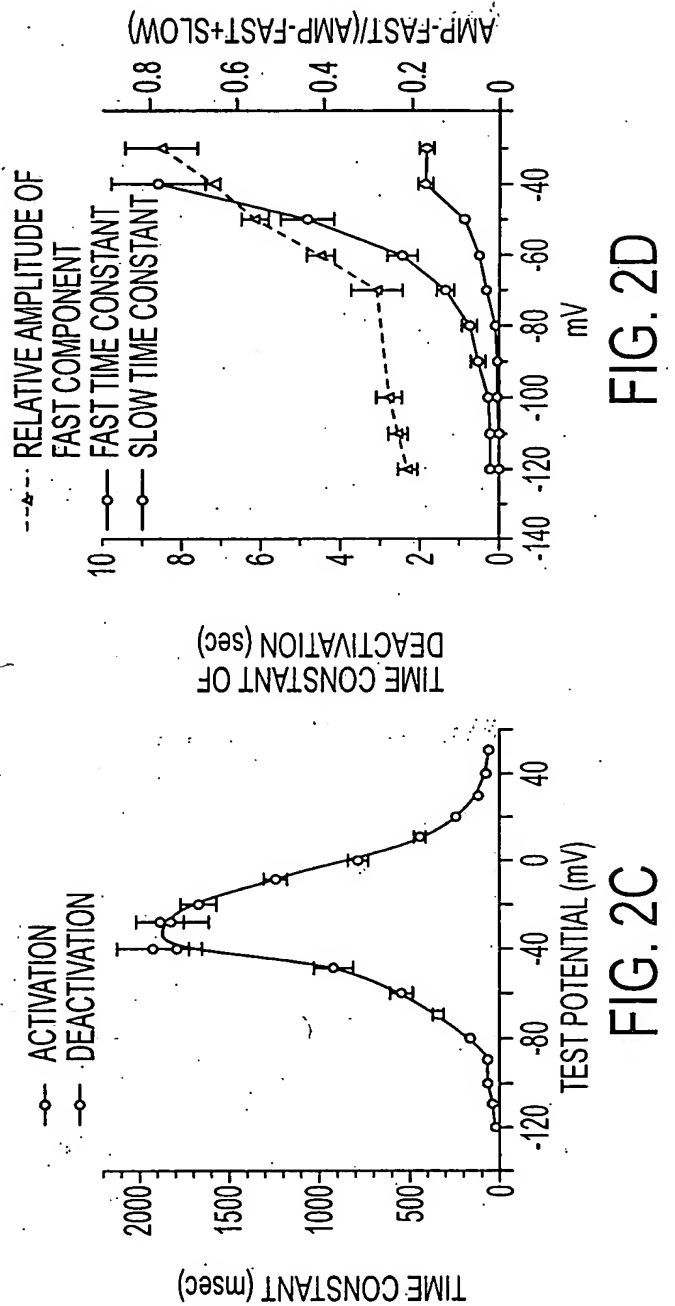
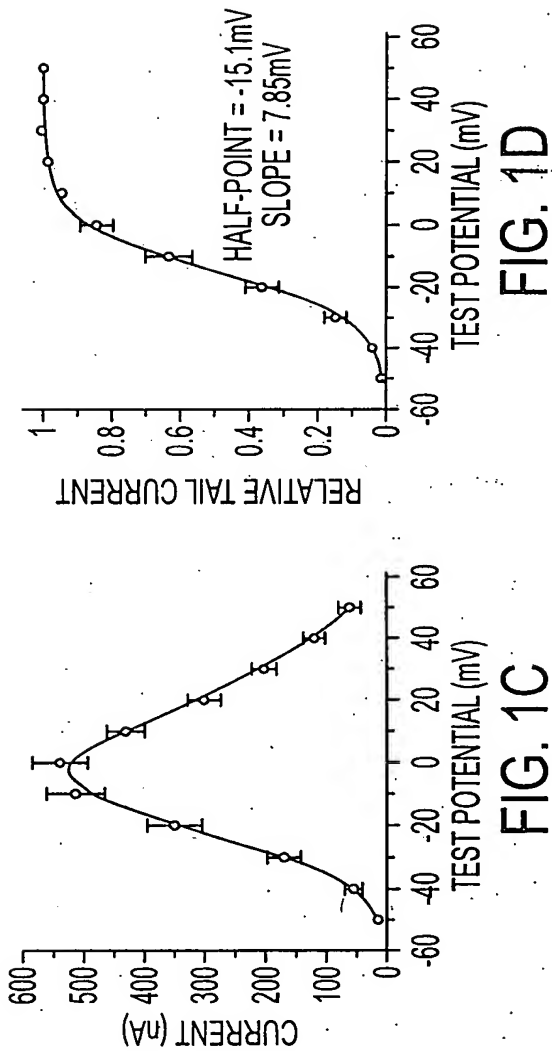


FIG. 1B



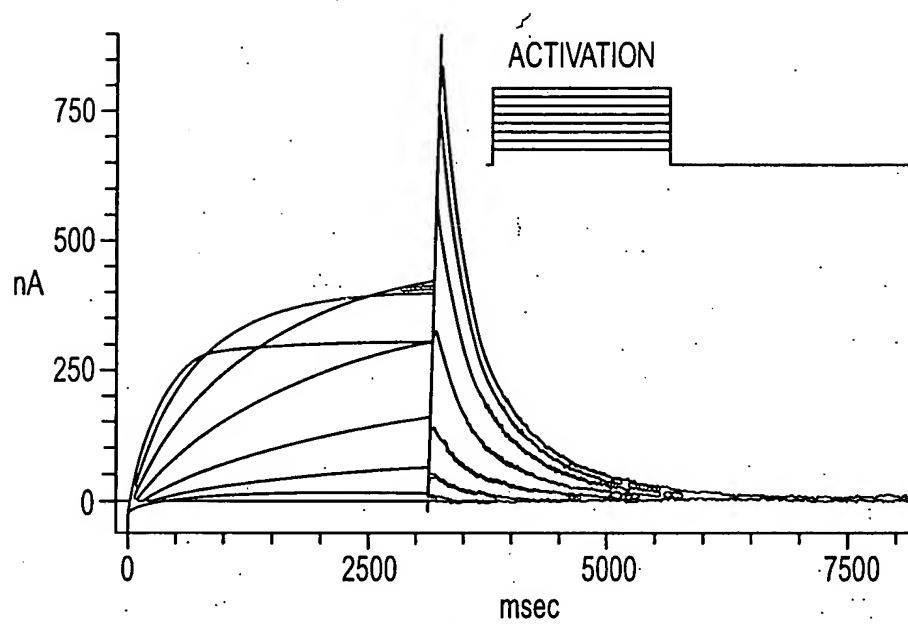


FIG. 2A

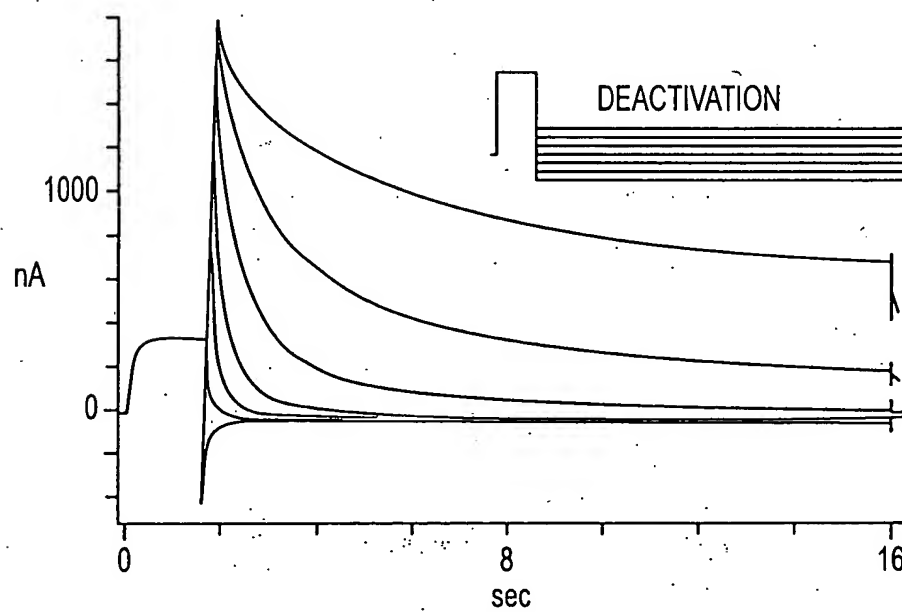


FIG. 2B

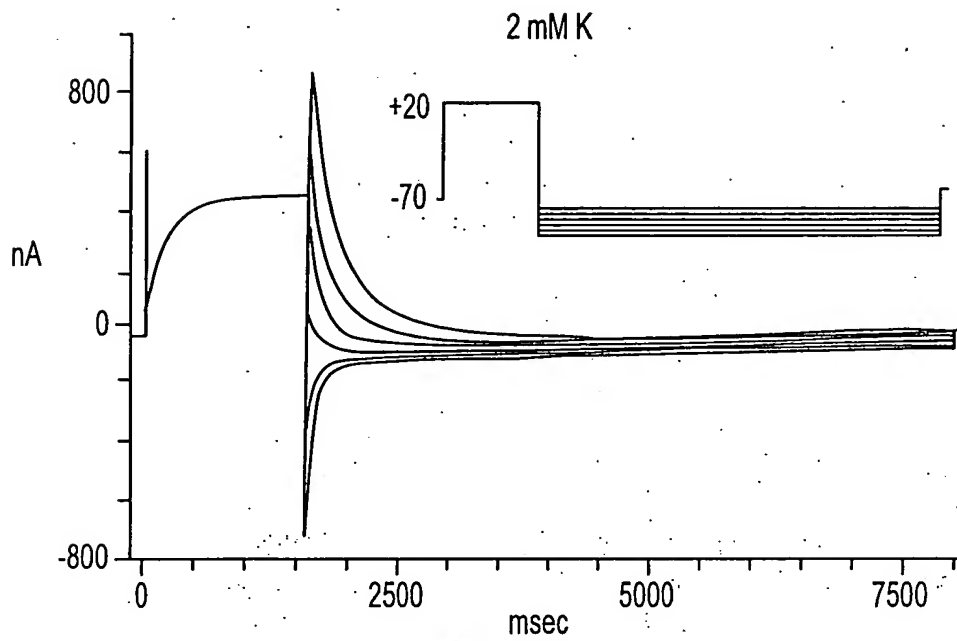


FIG. 3A

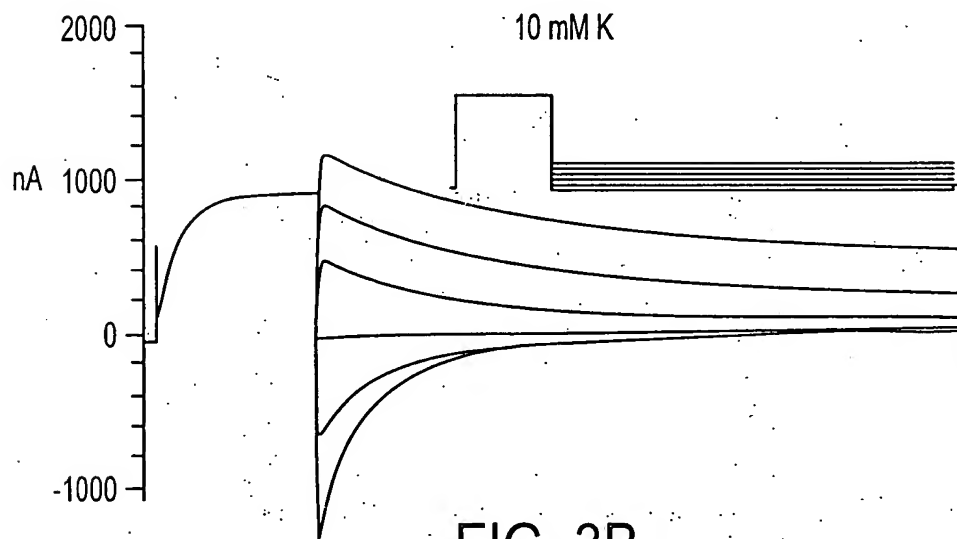


FIG. 3B

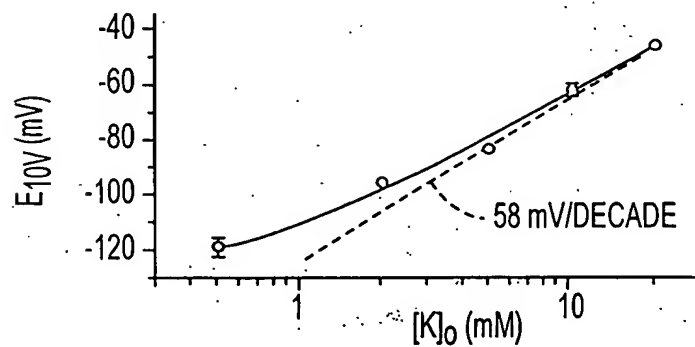


FIG. 3C

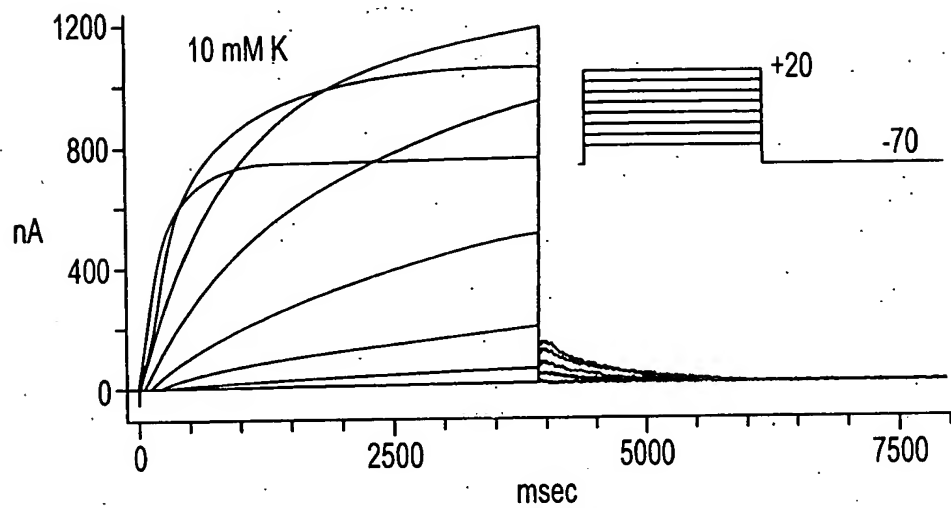


FIG. 4A

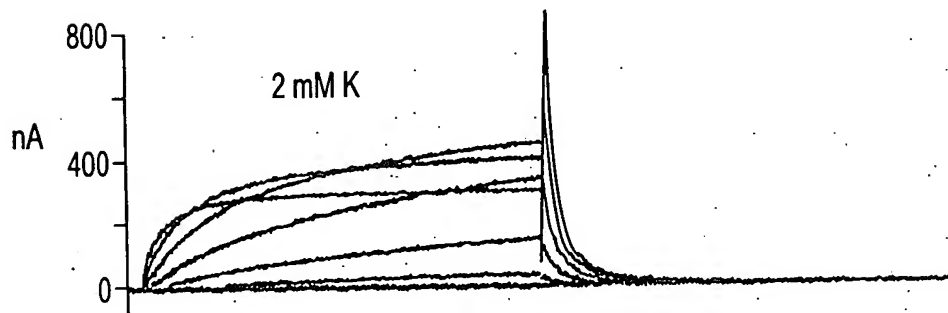


FIG. 4B

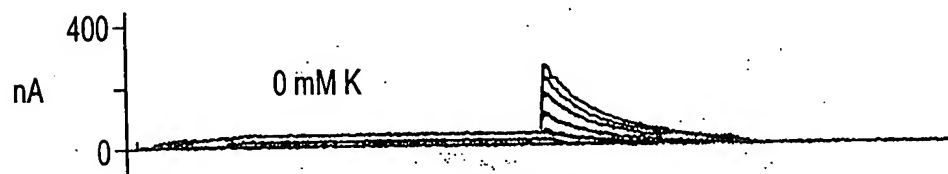


FIG. 4C

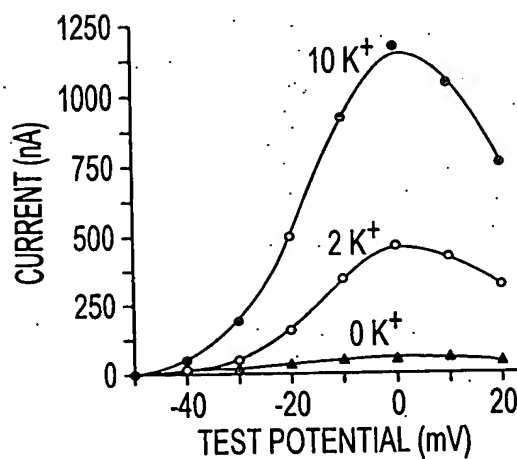


FIG. 4D

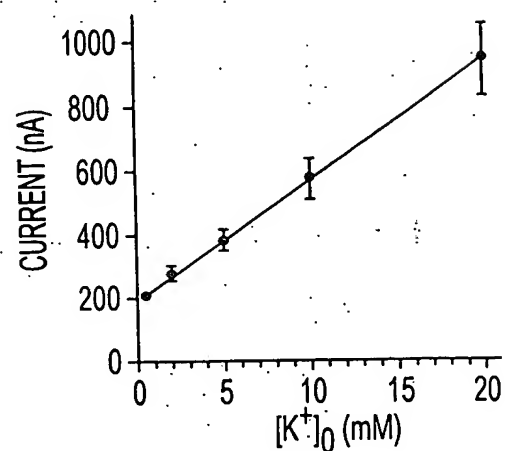


FIG. 4E

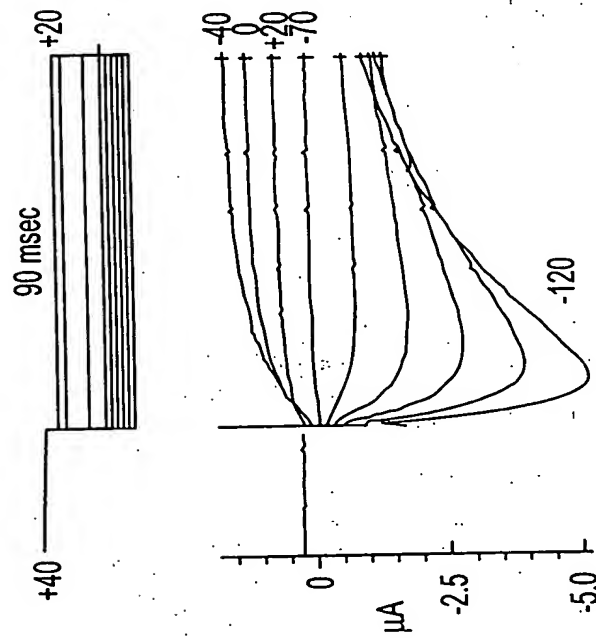


FIG. 5A

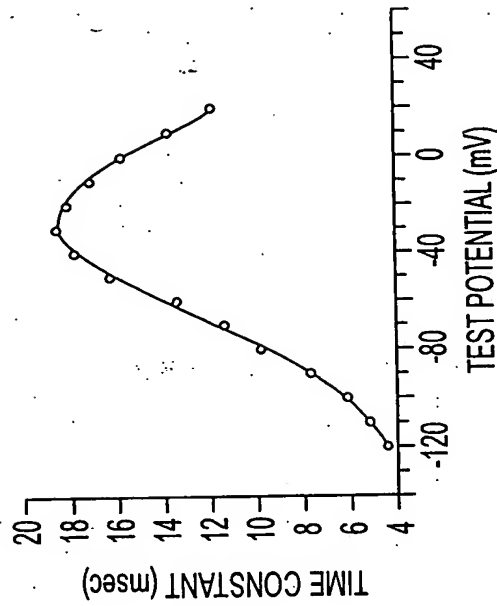


FIG. 5B

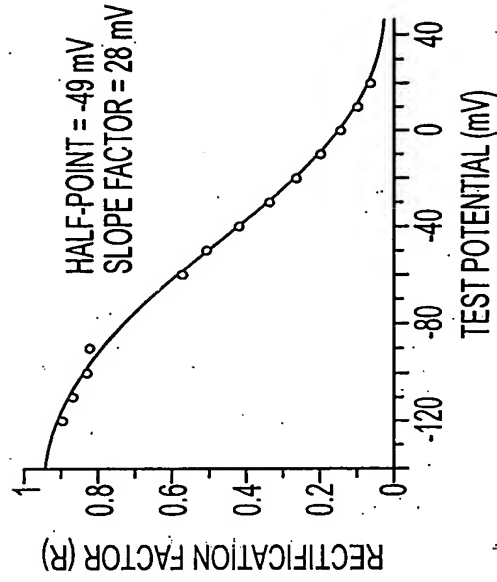


FIG. 5D

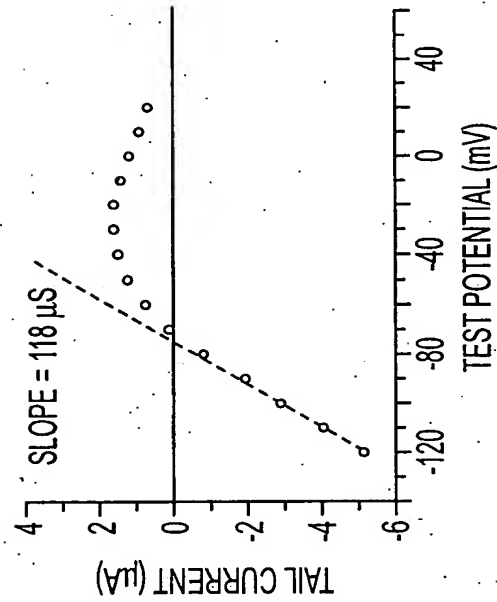


FIG. 5C

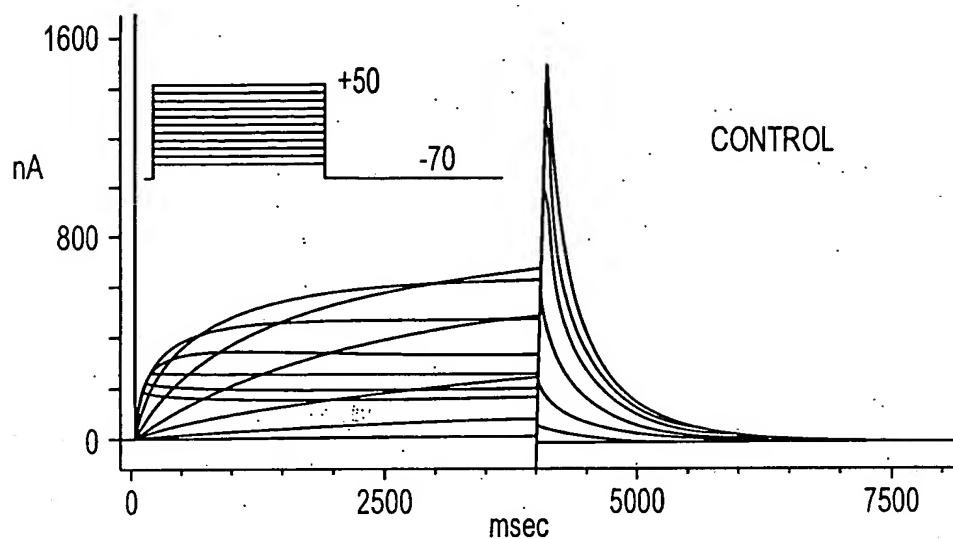


FIG. 6A

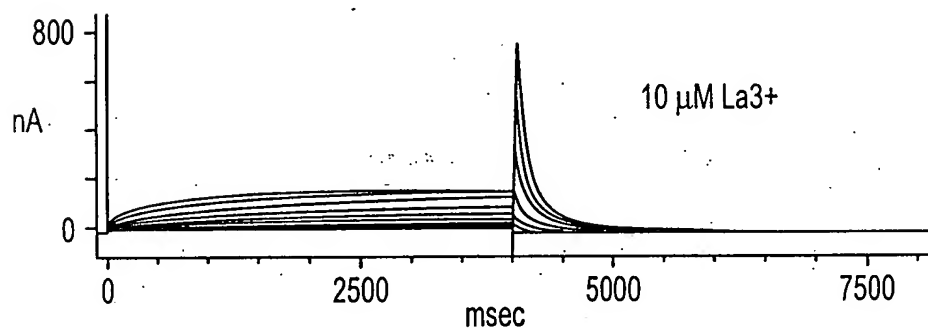


FIG. 6B

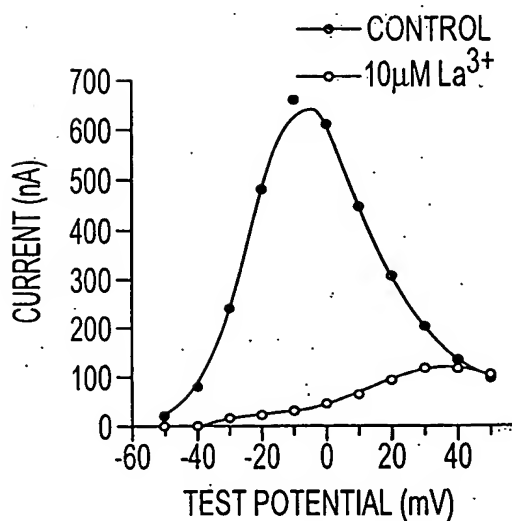


FIG. 6C

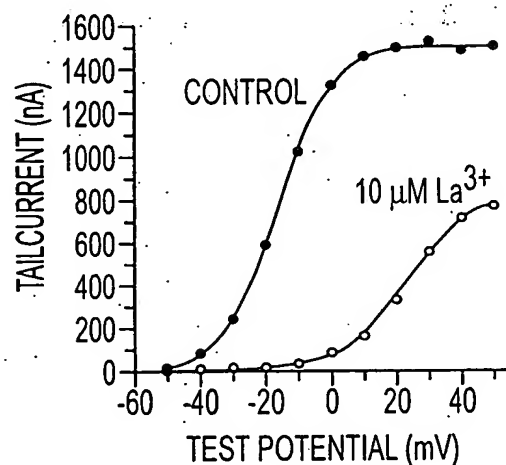


FIG. 6D



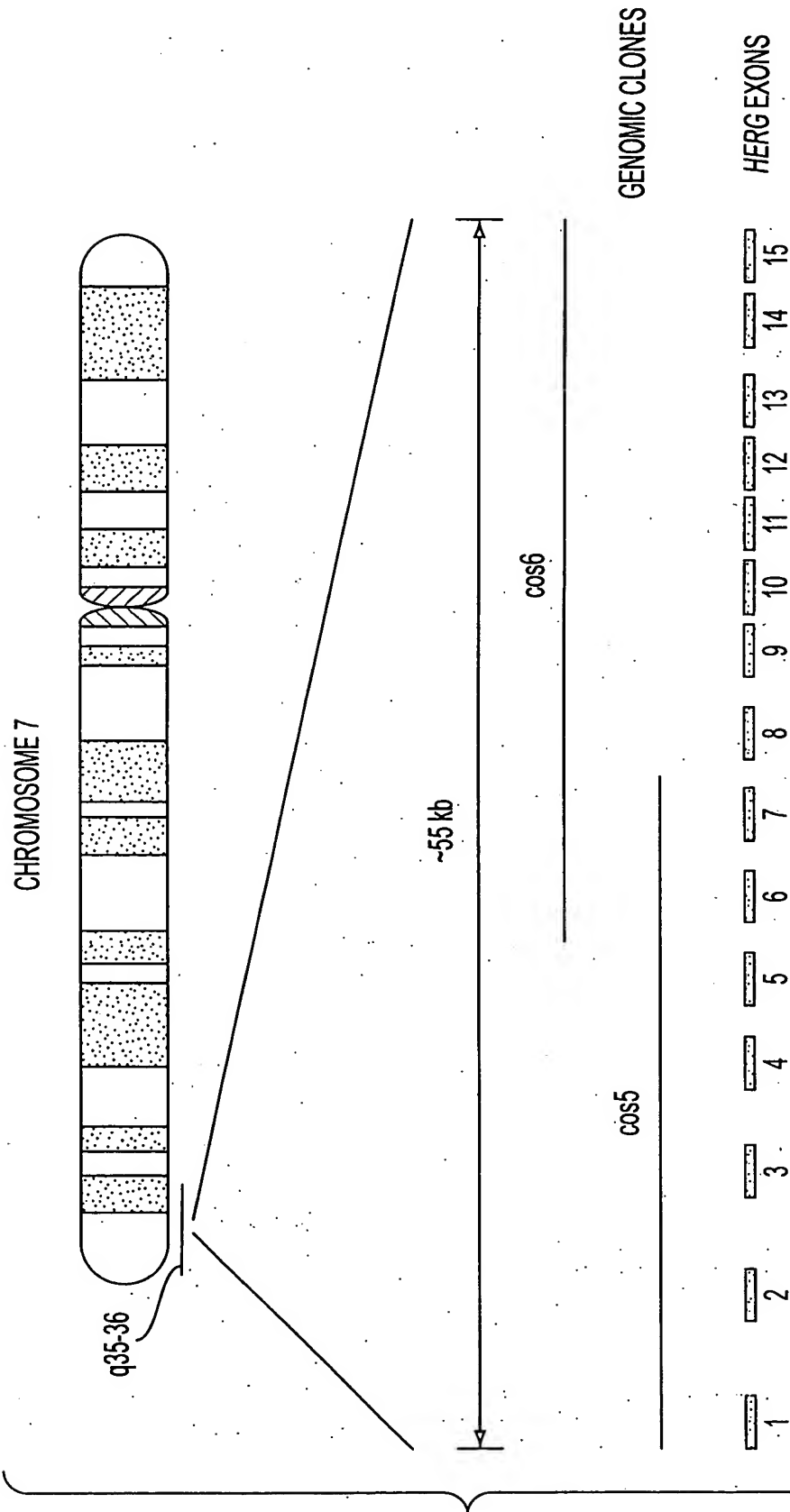


FIG. 7

AGCCTAGTGCTGGGCCGGGCCGGGGTGGGTGGGGCCCGCCCGCCATGGGCTAGGATGCCGAGGAGG-81  
 GGGCACGTCGCGCCGAGAACACCTTCTGACACCATCATCCGAAGTTTGAGGGCCAGAGCCGTAAGTTCATCATCGCC-162  
 G H V A P Q N T F L D T I I R K F E G Q S R K F I I A -32  
 AACGCTCGGGTGGAGAACTGCGCCGTCATCTACTGCAACGACGGCTTCTGCGAGCTGTGCGGCTACTCGCGGGCCGAGGTG-243  
 N A R V E N C A V I Y C N D G F C E L C G Y S R A E V -59  
 ATGCAGCGACCTGCACCTGCGACTTCTCTGCACGGCCGCGCAGCGAGCCGCGCTGCCGCGCAGATCCGCGAGGACATG-324  
 M Q R P C T C D F L H G P R T Q R R A A A Q I A Q A L -86  
 CTGGGCGCCGAGGAGCGCAAAGTGAAATCGCCTTCTACCGAAAGATGGGAGCTGCTTCTATGTCTGGTGGATGTGGTG-405  
 L G A E E R K V E I A F Y R K D G S C F L C L V D V V -113  
 CCCGTGAAGAACGAGGATGGGGCTGTCTATCATGTTTCATCCTCAATTTTCAGGTGGTGATGGAGAAGGACATGGTGGGGTCC-486  
 P V K N E D G A V I M F I L N F E V V M E K D M V G S -140  
 CCGGCTCATGACACCAACCACCGGGGCCCCCACCAGCTGGCTGGCCCCAGGCCGCGCAAGACCTTCCGCCTGAAGCTG-567  
 P A H D T N H R G P P T S W L A P G R A K T F R L K L -167  
 CCCGCGCTGCTGCGCTGACGGCCCGGAGTCGTCGCTGCGGTGCGGCGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGG-648  
 P A L L A L T A R E S S V R S G G A G G A G A P G A V -194  
 GTGGTGGACGTGGACCTGACGCCGCGGACCCAGCAGCGAGTCGCTGGCCCTGGACGAAGTGACAGCCATGGACACAC-729  
 V V D V D L T P A A P S S E S L A L D E V T A M D N H -221  
 GTGGCAGGGCTCGGGCCCGGAGGAGCGGCGTGCCTGGTGGGTCCCGGCTCTCCGCCCCGAGCGCGCCCGGCCAGCTC-810  
 V A G L G P A E E R R A L V G P G S P P R S A P G Q L -248  
 CCATCGCCCCGGGCGCACAGCCTCAACCCGACGCTCGGGCTCCAGCTGCAGCCTGGCCCGGACGCGCTCCCGAGAAAGC-891  
 P S P R A H S L N P D A S G S S C S L A R T R S R E S -275  
 TCGCCAGCGTGCGCCGCGCTCGTCGGCCGACGACATCGAGGCCATGCGCGCGGGGTGCTGCCCGGCCACCGCGCCAC-972  
 C A S V R R A S S A D D I E A M R A G V L P P P P R H -302  
 GCCAGCACCGGGCCATGCACCCACTGCGCAGCGGCTTGCTCAACTCCACCTCGGACTCCGACCTCGTGCGCTACCGCACC-1053  
 A S T G A M H P L R S G L L N S T S D S D L V R Y R T -329  
 ATTAGCAAGATTCCCAAATCACCTCAACTTTGTGGACCTCAAGGGCGACCCCTTCTTGGCTTCGCCACCAAGTGACCGT-1134  
 I S K I P Q I T L N F V D L K G D P F L A S P T S D R -356  
 GAGATCATAGCACCTAAGATAAAGGAGCGAACCACAATGTCACTGAGAAGGTCACCCAGGTCTGTCCCTGGGCGCCGAC-1215  
 E I I A P K I K E R T H N V T E K V T Q V L S L G A D -383  
 GTGCTGCTGAGTACAAGCTGCAGGCACCGCGCATCCACCGCTGGACCATCTGCATTACAGCCCCCTCAAGGCCGTGTGG-1296  
 V L P E Y K L Q A P R I H R W T I L H Y S P F K A V W -410  
 GACTGGCTCATCTGCTGCTGGTTCATCTACACGGCTGTCTTACACCCCTACTCGGCTGCCTTCTGCTGAAGGAGACGGAA-1377  
 D W L I L L L V I Y T A V F T P Y S A A F L L K E T E -437  
 GAAGCCCCGCTGCTACCGAGTGTGGCTACGCCTGCCAGCCGCTGGCTGTGGTGGACCTCATCGTGGACATCATGTTTCATT-1458  
 E G P P A T E C G Y A C Q P L A V V D L I V D I M F I -464  
 GTGGACATCCTCATCAACTTCCGCACCACCTACGTCAATGCCAACGAGGAGGTGGTCAGCCACCCCGCCGCGCATCGCCGTC-1539  
 V D I L I N F R T T Y V N A N E E V V S H P G R I A V -491  
 CACTACTTCAAGGGTGGTTTCTCATCGACATGGTGGCCGCGCATCCCTTCGACCTGCTCATCTTCGGCTCTGGCTCTGAG-1620  
 H Y F K G W F L I D M V A A I P F D L L I F G S G S E -518  
 GAGCTGATCGGGCTGCTGAAGACTGCGCGGCTGCTGCGGCTGGTGGCGGTGGCGGGAAGCTGGATCGCTACTCAGAGTAC-1701  
 E L I G L L K T A R L L R L V R V A R K L D R Y S E Y -545  
 GGCGCGCCGCTGCTGTTCTTGCTCATGTGCACCTTTGCGCTCATCGCGCACTGGCTAGCCTGCATCTGGTACGCCATCGGC-1782  
 G A A V L F L L M C T F A L I A H W L A C I W Y A I G -572  
 AACATGGAGCAGCCACACATGGACTCACGCATCGGCTGGCTGCACAACCTGGGCGACCAGATAGGCAAACCTTACAACAGC-1863  
 N M E Q P H M D S R I G W L H N L G D Q I G K P Y N S -599  
 AGCGGCTGGGCGGCCCCCTCCATCAAGGACAAGTATGTACGGCGCTCTACTTACCTTTCAGCAGCCTCACCAGTGTGGGC-1944  
 S G L G G P S I K D K Y V T A L Y F T F S S L T S V G -626  
 TTCGGCAACGTCTCTCCCAACCAACTCAGAGAAGATCTTCTCCATCTGCGTCATGCTCATTGGCTCCCTCATGTATGCT-2025  
 F G N V S P N T N S E K I F S I C V M L I G S L M Y A -653

FIG. 8A

AGCATCTTCGGCAACGTGTGCGCCATCATCCAGCGGCTGTACTCGGGCACAGCCGCTACCACACACAGATGCTGCGGGTG-2106  
 S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTTCATCCGCTTCCACCAGATCCCCAATCCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCTGGTCTTAC-2187  
 R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707

▽

ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268  
 T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734  
 TCACTGCTGCAGCACTGCAAACCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGCGCTGGCCATGAAGTTCAAGACCACA-2349  
 S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761  
 CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGGACCTGCTCACCGCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430  
 H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788

▽

ATCCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511  
 I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815

cNBD

GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTGCTG-2592  
 G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842

▽

GACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673  
 D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869  
 GGCTCCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGTCTTCCGAGGCGCACGGAC-2754  
 G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896

▽

AAGGACACGGAGCAGCCAGGGGAGGTGTGCGCCTTGGGGCCGGGCGGGGCGGGGCGAGGCGGAGTAGCCGGGGCCGGCCG-2835  
 K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923  
 GGGGGGCGGTGGGGGAGAGCCCGTCCAGTGGCCCCCTCAGCCCTGAGAGCAGTGAGGATGAGGGCCAGGCCGAGCTCC-2916  
 G G P W G E S P S S G P S S P E S S E D E G P G R S S -950  
 AGCCCCCTCCGCTGGTGGCCTTCTCCAGCCCCAGGCCCCCGGAGAGCCGCGGGTGGGGAGCCCTGATGGAGGACTGC-2997  
 S P L R L V P F S S P R P P G E P P G G E P L M E D C -977

▽

GAGAAGAGCAGCGACACTTGCAACCCCTGTGAGGCGCCTTCTCAGGAGTGTCCAACATTTTCAGCTTCTGGGGGACAGT-3078  
 E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004  
 CGGGGCGCCAGTACCAGGAGCTCCCTCGATGCCCCGCCCCACCCCCAGCCTCCTCAACATCCCCCTCTCCAGCCCGGT-3159  
 R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031

▽

CGGCGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240  
 R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058  
 GACATGGCCACTGTCTGTCAGCTGCTACAGAGGCAGATGACGCTGGTCCGCGCCGCTACAGTGTGTGACCACCCCGGG-3321  
 D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085

▽

CCTGGCCCCACTTCCACATCCCCGCTGTTGCCCGTCAGCCCCCTCCCCACCCTCACCTTGGACTCGCTTCTCAGGTTTCC-3402  
 P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112  
 CAGTTTCATGGCGTGTGAGGAGTGGCCCCGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCTCTCCCTACCG-3483  
 Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139  
 GGCCAGCTGGGGGCCCTCACCTCCCAGCCCCGTCACAGACACGGCTCGGACCCGGGAGTTAGTGGGGCTGCCAGTGTGG-3564  
 G Q L G A L T S Q P L H R H G S D P G S \* -1159  
 ACACGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGCGCTCCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCGTGGAAG-3645  
 GGGAGAGGAACTCGAAAGCACAGCTCCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCTGGGCCCCAGTGAGAG-3726  
 GGGCAGGGGCGAGGCGGCGAGTAGGTGGGCGCTGTGGTCCCCCATGCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807  
 GGCACCCGCGCTGGGCGCTTGGCACCTCAAGGACTTTCTGCTATTACTGCTCTTATTGTTAAGGATAATAATTAAGGA-3888  
 TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATTATCCTGAGGAG (A) n -3949

FIG. 8B

K2287

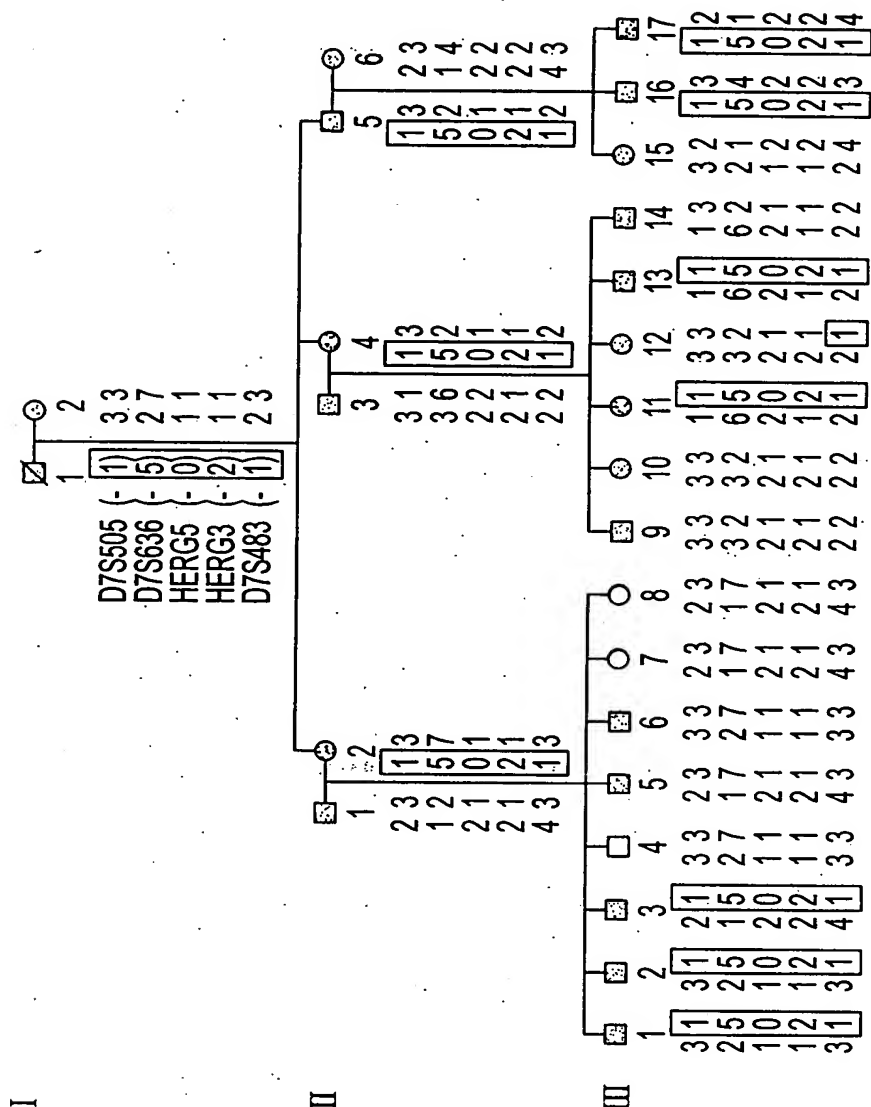


FIG. 9B

K1956

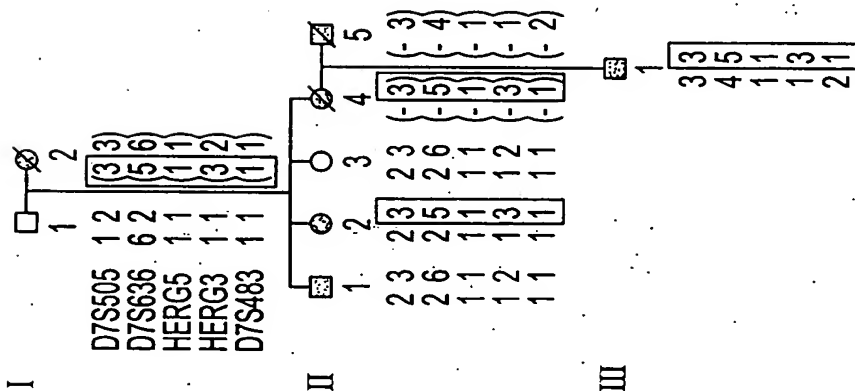


FIG. 9A

FIG. 6E

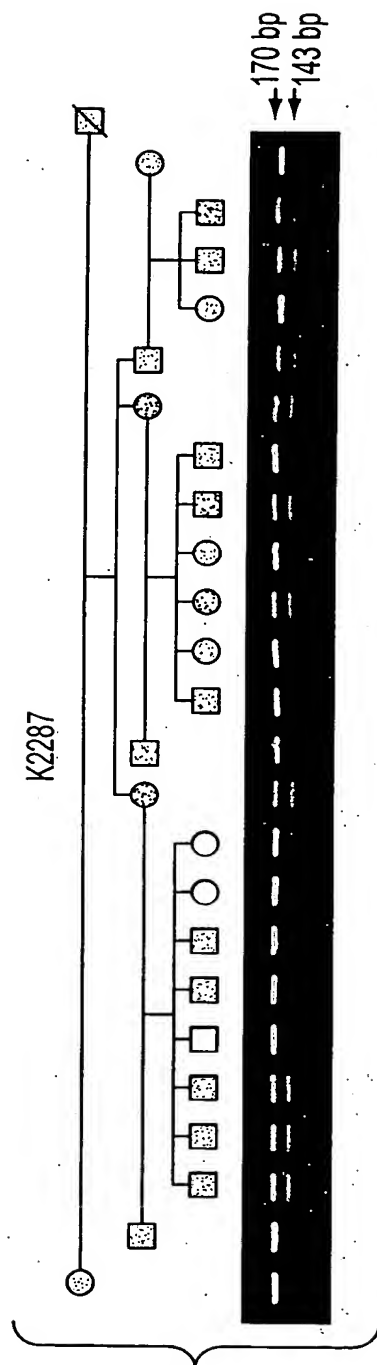


FIG. 10A

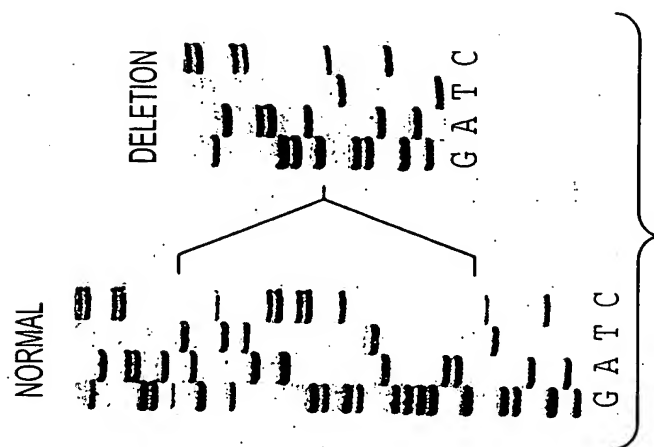


FIG. 10B

TGG TTC CTC ATC GAC ATG GTG GCC GCC ATC CCC TTC GAC CTG CTC SEQ ID NO:96  
 W F L I D M V A A I P F D L L SEQ ID NO:97  
 S3

FIG. 10C

NORMAL GTC ATC TAC ACG GGT GTC TTC ACA CCC TAC TCG GCT GCC TTC CTG CTG AAG GAG SEQ ID NO:98  
 V I Y T A V F T P Y S A A F L L K E SEQ ID NO:99

DELETION GTC ATC TAC CGG CTG TCT TCA CAC CCT ACT CGG CTG CCT TCC TGC TGA SEQ ID NO:100  
 V I Y R L S S S H P T R L P S C SEQ ID NO:101

FIG. 11C

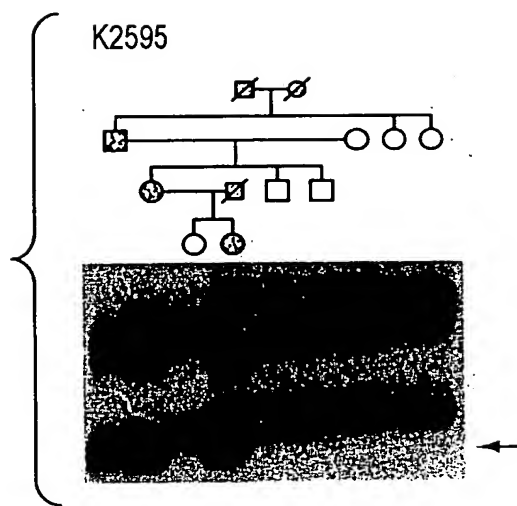


FIG. 11A

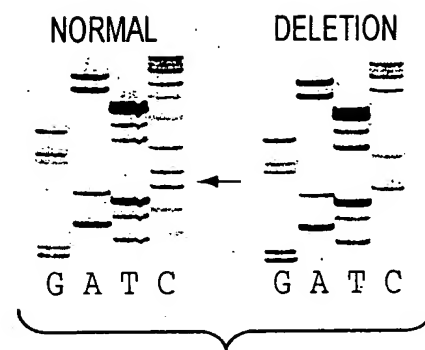


FIG. 11B



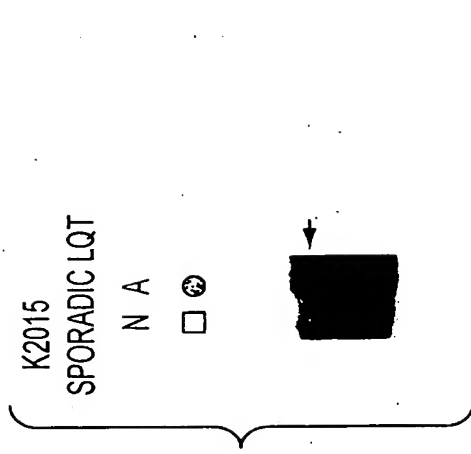


FIG. 12E

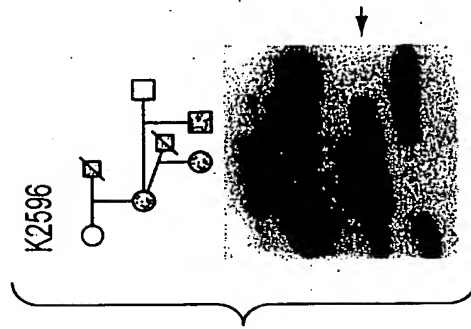


FIG. 12C

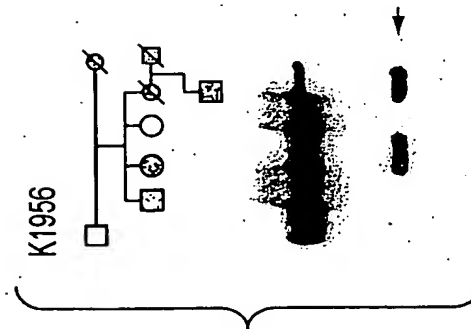


FIG. 12A

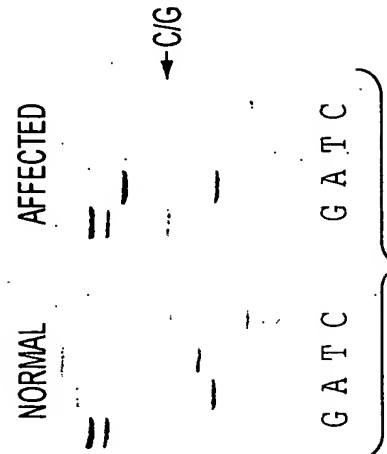


FIG. 12F

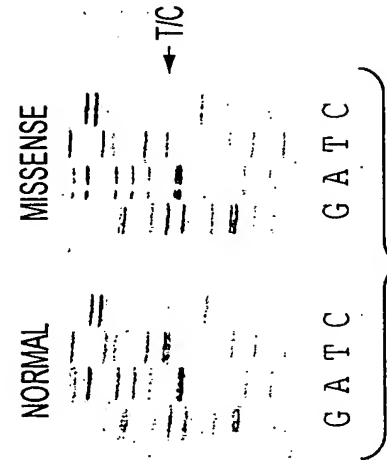


FIG. 12D

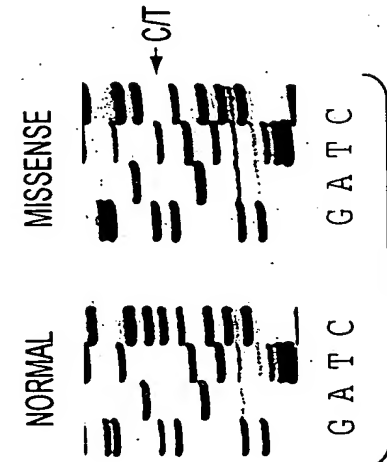


FIG. 12B

	GTG → V	SEQ ID NO:
	GCG	
	\\	
	L I A H W L	102
	↔ S5 ↔	
K1956	L I V H W L	103
H-Erg	L I A H W L	102
M-Eag	L A A H W K	104
R-Eag	L A A H W M	105
Eag	L V A H W L	106
Elk	L A A H W L	107

	GAC → D	SEQ ID NO:
	AAC	
	\\	
	D I L I N F R	108
	↔ S2 ↔	
K2596	D I L I D F R	109
H-Erg	D I L I N F R	108
M-Eag	D I V L N F H	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I L L N F R	111

FIG. 12G

FIG. 12H

5'-CAT CCT GG // gtagggg-3'  
 ↓  
 C

FIG. 12I

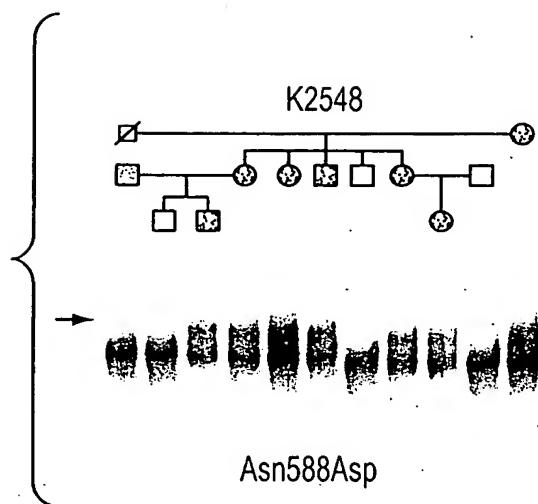


FIG. 13A

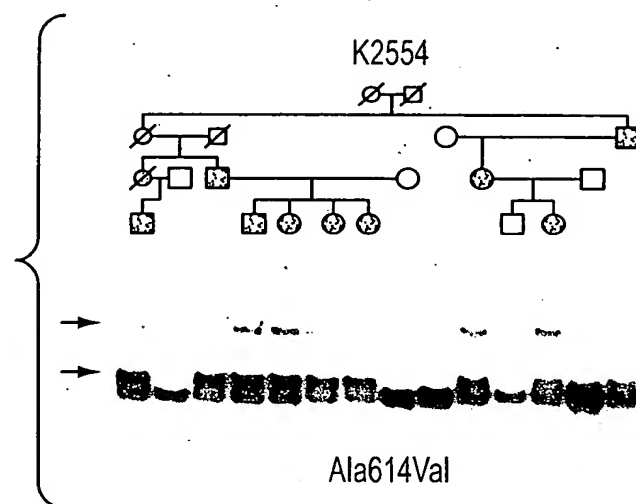


FIG. 13B

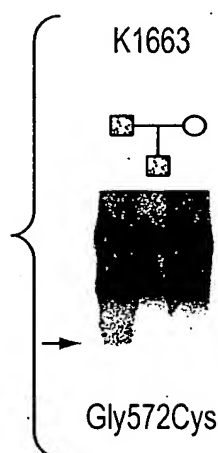


FIG. 13C

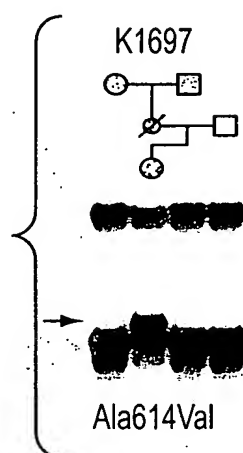


FIG. 13D

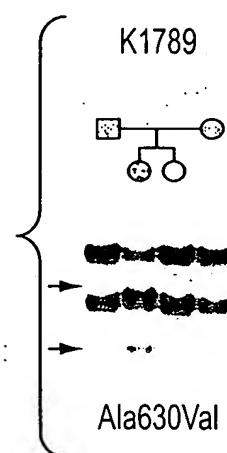


FIG. 13E

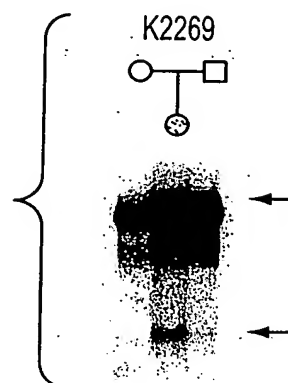


FIG. 14A

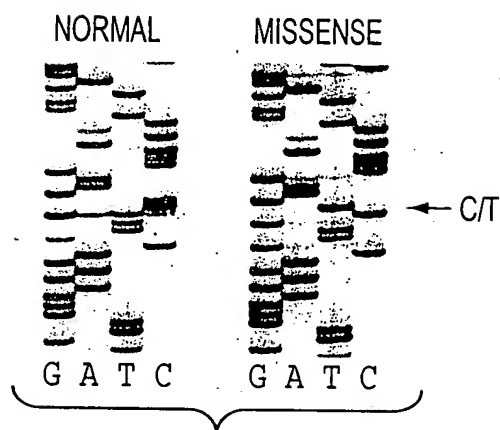


FIG. 14B

	AGC → S	SEQ ID
	GGC	NO:
	SVGFGNVS	112
	← PORE →	
K2269	SVGFSNVS	113
H-Erg	SVGFGNVS	112
M-Eag	SVGFGNIA	114
R-Eag	SVGFGNIA	114
Eag	SVGFGNVA	115
Elk	SVGFGNVS	112
Shaker	TVGYGDMT	116

FIG. 14C

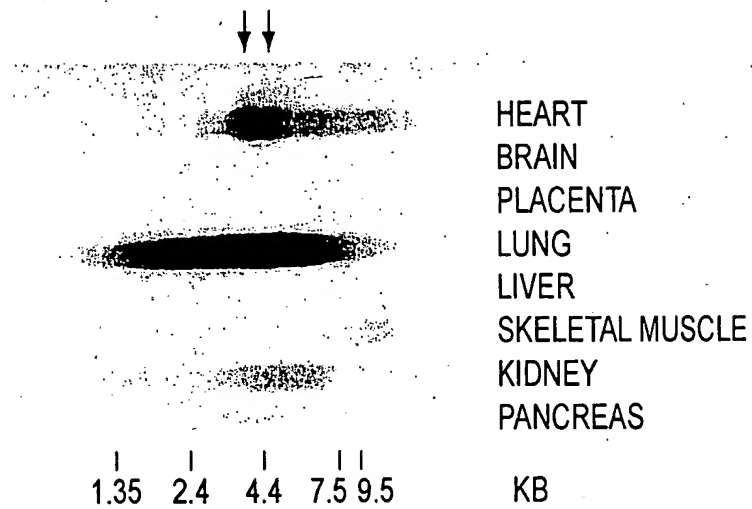


FIG. 15